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JUL 02 2003

TECH CENTER



1600

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/647,140B

DATE: 06/23/2003

TIME: 14:00:58

Input Set : A:\Kruh 140 SequenceListing v2.txt  
 Output Set: N:\CRF4\06232003\I647140B.raw

3 <110> APPLICANT: Fox Chase Cancer Center  
 4 Kruh, Gary D.  
 5 Lee, Kun  
 6 Belinsky, Martin G.  
 7 Bain, Lisa J.  
 9 <120> TITLE OF INVENTION: MRP-Related ABC Transporter Encoding  
 10 Nucleic Acids and Methods of Use Thereof  
 12 <130> FILE REFERENCE: FCCC 98-02  
 14 <140> CURRENT APPLICATION NUMBER: 09/647,140B  
 15 <141> CURRENT FILING DATE: 2001-05-21  
 17 <150> PRIOR APPLICATION NUMBER: PCT/US99/06644  
 18 <151> PRIOR FILING DATE: 1999-03-26  
 20 <150> PRIOR APPLICATION NUMBER: 60/079,759  
 21 <151> PRIOR FILING DATE: 1998-03-27  
 23 <150> PRIOR APPLICATION NUMBER: 60/095,153  
 24 <151> PRIOR FILING DATE: 1998-08-03  
 26 <160> NUMBER OF SEQ ID NOS: 33  
 28 <170> SOFTWARE: FastSEQ for Windows Version 3.0  
 31 <210> SEQ ID NO: 1  
 32 <211> LENGTH: 4231  
 33 <212> TYPE: DNA  
 34 <213> ORGANISM: Homo sapiens  
 36 <400> SEQUENCE: 1

P.6

ENTERED

37	ggacaggcgt	ggcgccgga	gccccagcat	ccctgcttga	ggtccaggag	cgagccccgc	60
38	ggccaccggc	gcctgatcag	cgcgaccccg	gccccggccc	gccccggcccg	gcaagatgct	120
39	gcccgtgtac	caggaggtga	agcccaaccc	gctgcaggac	gcgaacatct	gctcagcgt	180
40	gttcttctgg	tggctcaatc	cctgtttaa	aattggccat	aaacggagat	tagaggaaga	240
41	tgatatgtat	tcagtgctgc	cagaagacccg	ctcacagcac	cttggagagg	agttgcaagg	300
42	gttctggat	aaagaagttt	taagagctga	gaatgacgca	cagaaggcctt	ctttaacaag	360
43	agcaatcata	aagtgttact	ggaaatctta	tttagttttg	gaaattttta	cgttaattga	420
44	ggaaagtgcc	aaagtaatcc	agcccatatt	tttggaaaaa	attattaatt	attttgaaaa	480
45	ttatgatccc	atggattctg	tggcttga	cacacgtac	gcctatgcca	cggtgctgac	540
46	ttttgcacg	ctcattttgg	ctatactgca	tcacttat	ttttatcacg	ttcagtgtgc	600
47	tggatgagg	ttacagtag	ccatgtgcca	tatgattt	cggaaggcac	ttcgtcttag	660
48	taacatggcc	atgggaaga	caaccacagg	ccagatagtc	aatctgctgt	ccaatgatgt	720
49	gaacaagttt	gatcaggtga	cagtgttctt	acacttcctg	tggcaggac	cactgcaggc	780
50	gatcgcagtg	actgccctac	tctggatgga	gataggaata	tcgtgccttgc	ctggatggc	840
51	agttctaattc	attctccctgc	ccttgcaaaag	ctgttttggg	aagttgttct	catcaactgag	900
52	gagtaaaact	gcaactttca	cggatgccag	gatcaggacc	atgaatgaag	ttataactgg	960
53	tataaggata	ataaaaatgt	acgcctggaa	aaagtcattt	tcaaatttctt	ttaccaattt	1020
54	gagaaagaag	gagatttcca	agattctgag	aaagtccctgc	ctcaggggga	tgaatttggc	1080
55	ttcgttttc	agtgaagca	aaatcatctgt	gtttgtgacc	ttcaccacat	acgtgctcct	1140
56	ccgcagtgtg	atcacagcca	gccgcgtt	cgtggcagtg	acgctgtat	gggctgtgcg	1200

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57	gctgacgggtt	accctcttct	tcggccatcgc	cattgagagg	gtgtcagagg	caatcgtcag	1260
58	catccgaaga	atccagacct	ttttgtact	tgatgagata	tcacagcgca	accgtcagct	1320
59	gcccgtcagat	ggtaaaaaaga	ttgtgcgtat	gcagatttt	actgttttt	gggataaggc	1380
60	atcagagacc	ccaactctac	aaggccttc	cttactgtc	agacctggcg	aattgttagc	1440
61	tgtggtcggc	cccgtggag	caggaaagtc	atcactgtt	agtgcgtgc	tcggggatt	1500
62	ggccccaagt	cacgggctgg	tcagcgtgca	tggaagaatt	gcctatgtgt	ctcagcagcc	1560
63	ctgggtgttc	tcgggaaactc	tgaggagtaa	tattttattt	gggaagaaat	ataaaaagga	1620
64	acatatgaa	aaagtataa	aggctgtgc	tctgaaaaag	gatttacagc	tgtggagga	1680
65	tgtgtatctg	actgtatag	gagatcgaaa	aaccacgctg	agtggagggc	agaaagcacf	1740
66	gttaaacctt	gcaagagcg	tgtatcaaga	tgctgacatc	tatctcctgg	acgatcctct	1800
67	cagtgcagta	gatgcggaa	ttagcagaca	cttggcgaa	ctgtgttattt	gtcaaatttt	1860
68	gcatgagaag	atcacaattt	tagtgactca	tcagttgcag	tacctcaaaag	ctgcaagtca	1920
69	gattctgata	ttgaaagatg	gtaaaatgt	gcagaagggg	acttacactg	agttcctaaa	1980
70	atctggata	gattttggct	cccttttaaa	gaaggataat	gaggaaatgt	aacaacctcc	2040
71	agttccagga	actccacac	taaggaatcg	tacttctca	gagtttcgg	tttggctca	2100
72	acaatcttct	agaccctcct	tgaaagatgg	tgctctggag	agccaagata	cagagaatgt	2160
73	cccagttaca	ctatcagagg	agaaccgttc	tgaaggaaaa	gttggtttc	aggcctataa	2220
74	gaattacttc	agagctggg	ctcactggat	tgtcttcatt	ttccttattt	tcctaaacac	2280
75	tgtagctcag	gttgccatg	tgcttcaaga	ttggggctt	tcataactggg	caaacaacaca	2340
76	aagtatgta	aatgtactg	taaatggagg	aggaaatgt	accgagaagc	tagatcttaa	2400
77	ctggacttta	ggaattttt	caggtttaac	tgttagctacc	gttcttttg	gcatagcaag	2460
78	atctctattt	gtattctacg	tccttggtaa	ctcttcacaa	actttgcaca	acaaaatgtt	2520
79	ttagtcaatt	ctgaaagctc	cggttatttt	ctttgataga	aatccaatag	gaagaatttt	2580
80	aaatcgtttc	tccaaagaca	ttggacactt	ggatgattt	ctgcccgtga	cgtttttaga	2640
81	tttcatccag	acattgctac	aagtgggtgg	tgtggctct	gtggctgtgg	ccgtgattcc	2700
82	ttggatcgca	atacccttgg	ttccccttgg	aatcattttc	attttcttc	ggcgatattt	2760
83	tttggaaacg	tcaagagatg	tgaagcgct	ggaatctaca	actcggagtc	cagtgtttc	2820
84	ccacttgtca	tcttctctcc	aggggctctg	gaccatccgg	gcatacaaag	cagaagagag	2880
85	gtgtcaggaa	ctgttgcgt	cacaccaggaa	tttacattca	gaggcttgg	tcttggttt	2940
86	gacaacgtcc	cgctgttgc	ccgtccgtct	ggatgccatc	tgtgccatgt	ttgtcatcat	3000
87	cgttgcctt	gggtccctga	ttctggcaaa	aactctggat	gccgggcagg	ttgttttggc	3060
88	actgtcctat	gccctcacgc	tcatggggat	gtttcagtgg	tgtgttcgac	aaagtgtctga	3120
89	agttgagaat	atgatgatct	cagtagaaag	ggtcattgaa	tacacagacc	ttgaaaaaaga	3180
90	agcaccttgg	gaatatcaga	aacgcccacc	accagcctgg	ccccatgaag	gagtgataat	3240
91	ctttgacaat	gtgaacttca	tgtacagttc	aggtgggcct	ctggacttga	agcatctgac	3300
92	agactctattt	aaatcacaag	aaaagggtgg	cattgtggga	agaaccggag	ctgaaaaaag	3360
93	ttccctcatc	tcagccctt	tttagattgtc	agaacccgaa	ggtaaaattt	ggattgataa	3420
94	gatcttgaca	actgaaattt	gacttcacga	tttaaggaag	aaaatgtcaa	tcatacctca	3480
95	ggaacctgtt	ttgttcactg	gaacaatgag	gaaaaacctg	gatcccttta	aggagcacac	3540
96	ggtatggagaa	ctgtggatg	ccttacaaga	ggtacaactt	aaagaaacca	ttgaagatct	3600
97	tcttggtaaa	atggatactg	aatttagcaga	atcaggatcc	aattttatgt	ttggacaaag	3660
98	acaactgggt	tgccttgcca	gggcaattt	cagaaaaat	cagatattga	ttattgtat	3720
99	agcgacggca	aatgtggatc	caagaactga	tgagttataa	aaaaaaaa	tccgggagaa	3780
100	atttgccttac	tgccacgtgc	taaccattgc	acacagattt	aacaccattt	ttgacagcga	3840
101	caagataatg	gttttagatt	caggaagact	gaaagaatat	gatgagccgt	atgttttgct	3900
102	gaaaataaaa	gagagcctat	tttacaagat	ggtcaacaa	ctgggcagg	cagaagccgc	3960
103	tgcctctact	gaaacagcaa	aacaggtata	cttcaaaaga	aattatccac	atattggtca	4020
104	cactgaccac	atggttacaa	acacttccaa	tggacagccc	tcgacccattt	ctatttcga	4080
105	gacagcactg	tgaatccaac	caaaatgtca	agtccgttcc	gaaggcattt	tccactagtt	4140

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106 tttggactat gtaaaccaca ttgtactttt ttttactttg gcaacaata tttatacata 4200  
 107 caagatgcta gttcatttga atatttctcc c 4231  
 110 <210> SEQ ID NO: 2  
 111 <211> LENGTH: 1325  
 112 <212> TYPE: PRT  
 113 <213> ORGANISM: Homo sapiens  
 115 <400> SEQUENCE: 2  
 116 Met Leu Pro Val Tyr Gln Glu Val Lys Pro Asn Pro Leu Gln Asp Ala  
 117 1 5 10 15  
 118 Asn Ile Cys Ser Arg Val Phe Phe Trp Trp Leu Asn Pro Leu Phe Lys  
 119 20 25 30  
 120 Ile Gly His Lys Arg Arg Leu Glu Glu Asp Asp Met Tyr Ser Val Leu  
 121 35 40 45  
 122 Pro Glu Asp Arg Ser Gln His Leu Gly Glu Glu Leu Gln Gly Phe Trp  
 123 50 55 60  
 124 Asp Lys Glu Val Leu Arg Ala Glu Asn Asp Ala Gln Lys Pro Ser Leu  
 125 65 70 75 80  
 126 Thr Arg Ala Ile Ile Lys Cys Tyr Trp Lys Ser Tyr Leu Val Leu Gly  
 127 85 90 95  
 128 Ile Phe Thr Leu Ile Glu Glu Ser Ala Lys Val Ile Gln Pro Ile Phe  
 129 100 105 110  
 131 Leu Gly Lys Ile Ile Asn Tyr Phe Glu Asn Tyr Asp Pro Met Asp Ser  
 132 115 120 125  
 133 Val Ala Leu Asn Thr Ala Tyr Ala Tyr Ala Thr Val Leu Thr Phe Cys  
 134 130 135 140  
 135 Thr Leu Ile Leu Ala Ile Leu His His Leu Tyr Phe Tyr His Val Gln  
 136 145 150 155 160  
 137 Cys Ala Gly Met Arg Leu Arg Val Ala Met Cys His Met Ile Tyr Arg  
 138 165 170 175  
 139 Lys Ala Leu Arg Leu Ser Asn Met Ala Met Gly Lys Thr Thr Gly  
 140 180 185 190  
 141 Gln Ile Val Asn Leu Leu Ser Asn Asp Val Asn Lys Phe Asp Gln Val  
 142 195 200 205  
 143 Thr Val Phe Leu His Phe Leu Trp Ala Gly Pro Leu Gln Ala Ile Ala  
 144 210 215 220  
 145 Val Thr Ala Leu Leu Trp Met Glu Ile Gly Ile Ser Cys Leu Ala Gly  
 146 225 230 235 240  
 147 Met Ala Val Leu Ile Ile Leu Leu Pro Leu Gln Ser Cys Phe Gly Lys  
 148 245 250 255  
 149 Leu Phe Ser Ser Leu Arg Ser Lys Thr Ala Thr Phe Thr Asp Ala Arg  
 150 260 265 270  
 151 Ile Arg Thr Met Asn Glu Val Ile Thr Gly Ile Arg Ile Ile Lys Met  
 152 275 280 285  
 153 Tyr Ala Trp Glu Lys Ser Phe Ser Asn Leu Ile Thr Asn Leu Arg Lys  
 154 290 295 300  
 155 Lys Glu Ile Ser Lys Ile Leu Arg Ser Ser Cys Leu Arg Gly Met Asn  
 156 305 310 315 320  
 157 Leu Ala Ser Phe Phe Ser Ala Ser Lys Ile Ile Val Phe Val Thr Phe  
 158 325 330 335

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159 Thr Thr Tyr Val Leu Leu Gly Ser Val Ile Thr Ala Ser Arg Val Phe  
 160 340 345 350  
 161 Val Ala Val Thr Leu Tyr Gly Ala Val Arg Leu Thr Val Thr Leu Phe  
 162 355 360 365  
 163 Phe Pro Ser Ala Ile Glu Arg Val Ser Glu Ala Ile Val Ser Ile Arg  
 164 370 375 380  
 165 Arg Ile Gln Thr Phe Leu Leu Leu Asp Glu Ile Ser Gln Arg Asn Arg  
 166 385 390 395 400  
 167 Gln Leu Pro Ser Asp Gly Lys Lys Met Val His Val Gln Asp Phe Thr  
 168 405 410 415  
 169 Ala Phe Trp Asp Lys Ala Ser Glu Thr Pro Thr Leu Gln Gly Leu Ser  
 170 420 425 430  
 171 Phe Thr Val Arg Pro Gly Glu Leu Leu Ala Val Val Gly Pro Val Gly  
 172 435 440 445  
 173 Ala Gly Lys Ser Ser Leu Leu Ser Ala Val Leu Gly Glu Leu Ala Pro  
 174 450 455 460  
 175 Ser His Gly Leu Val Ser Val His Gly Arg Ile Ala Tyr Val Ser Gln  
 176 465 470 475 480  
 177 Gln Pro Trp Val Phe Ser Gly Thr Leu Arg Ser Asn Ile Leu Phe Gly  
 178 485 490 495  
 179 Lys Lys Tyr Glu Lys Glu Arg Tyr Glu Lys Val Ile Lys Ala Cys Ala  
 180 500 505 510  
 181 Leu Lys Lys Asp Leu Gln Leu Leu Glu Asp Gly Asp Leu Thr Val Ile  
 182 515 520 525  
 183 Gly Asp Arg Gly Thr Pro Leu Ser Gly Gly Gln Lys Ala Arg Val Asn  
 184 530 535 540  
 185 Leu Ala Arg Ala Val Tyr Gln Asp Ala Asp Ile Tyr Leu Leu Asp Asp  
 186 545 550 555 560  
 187 Pro Leu Ser Ala Val Asp Ala Glu Val Ser Arg His Leu Phe Glu Leu  
 188 565 570 575  
 189 Cys Ile Cys Gln Ile Leu His Glu Lys Ile Thr Ile Leu Val Thr His  
 190 580 585 590  
 191 Gln Leu Gln Tyr Leu Lys Ala Ala Ser Gln Ile Leu Ile Leu Lys Asp  
 192 595 600 605  
 193 Gly Lys Met Val Gln Lys Gly Thr Tyr Glu Phe Leu Lys Ser Gly  
 194 610 615 620  
 196 Ile Asp Phe Gly Ser Leu Leu Lys Lys Asp Asn Glu Glu Ser Glu Gln  
 197 625 630 635 640  
 198 Pro Pro Val Pro Gly Thr Pro Thr Leu Arg Asn Arg Thr Phe Ser Glu  
 199 645 650 655  
 200 Ser Ser Val Trp Ser Gln Gln Ser Ser Arg Pro Ser Leu Lys Asp Gly  
 201 660 665 670  
 202 Ala Leu Glu Ser Gln Asp Thr Glu Asn Val Pro Val Thr Leu Ser Glu  
 203 675 680 685  
 204 Glu Asn Arg Ser Glu Gly Lys Val Gly Phe Gln Ala Tyr Lys Asn Tyr  
 205 690 695 700  
 206 Phe Arg Ala Gly Ala His Trp Ile Val Phe Ile Phe Leu Ile Leu Leu  
 207 705 710 715 720  
 208 Asn Thr Ala Ala Gln Val Ala Tyr Val Leu Gln Asp Trp Trp Leu Ser

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209	725	730	735
210	Tyr Trp Ala Asn Lys Gln Ser Met Leu Asn Val Thr Val Asn Gly Gly		
211	740	745	750
212	Gly Asn Val Thr Glu Lys Leu Asp Leu Asn Trp Tyr Leu Gly Ile Tyr		
213	755	760	765
214	Ser Gly Leu Thr Val Ala Thr Val Leu Phe Gly Ile Ala Arg Ser Leu		
215	770	775	780
216	Leu Val Phe Tyr Val Leu Val Asn Ser Ser Gln Thr Leu His Asn Lys		
217	785	790	795
218	Met Phe Glu Ser Ile Leu Lys Ala Pro Val Leu Phe Phe Asp Arg Asn		
219	805	810	815
220	Pro Ile Gly Arg Ile Leu Asn Arg Phe Ser Lys Asp Ile Gly His Leu		
221	820	825	830
222	Asp Asp Leu Leu Pro Leu Thr Phe Leu Asp Phe Ile Gln Thr Leu Leu		
223	835	840	845
224	Gln Val Val Gly Val Val Ser Val Ala Val Ala Val Ile Pro Trp Ile		
225	850	855	860
226	Ala Ile Pro Leu Val Pro Leu Gly Ile Ile Phe Ile Phe Leu Arg Arg		
227	865	870	875
228	Tyr Phe Leu Glu Thr Ser Arg Asp Val Lys Arg Leu Glu Ser Thr Thr		
229	885	890	895
230	Arg Ser Pro Val Phe Ser His Leu Ser Ser Ser Leu Gln Gly Leu Trp		
231	900	905	910
232	Thr Ile Arg Ala Tyr Lys Ala Glu Glu Arg Cys Gln Glu Leu Phe Asp		
233	915	920	925
234	Ala His Gln Asp Leu His Ser Glu Ala Trp Phe Leu Phe Leu Thr Thr		
235	930	935	940
236	Ser Arg Trp Phe Ala Val Arg Leu Asp Ala Ile Cys Ala Met Phe Val		
237	945	950	955
238	Ile Ile Val Ala Phe Gly Ser Leu Ile Leu Ala Lys Thr Leu Asp Ala		
239	965	970	975
240	Gly Gln Val Gly Leu Ala Leu Ser Tyr Ala Leu Thr Leu Met Gly Met		
241	980	985	990
242	Phe Gln Trp Cys Val Arg Gln Ser Ala Glu Val Glu Asn Met Met Ile		
243	995	1000	1005
244	Ser Val Glu Arg Val Ile Glu Tyr Thr Asp Leu Glu Lys Glu Ala Pro		
245	1010	1015	1020
246	Trp Glu Tyr Gln Lys Arg Pro Pro Pro Ala Trp Pro His Glu Gly Val		
247	1025	1030	1035
248	Ile Ile Phe Asp Asn Val Asn Phe Met Tyr Ser Pro Gly Gly Pro Leu		
249	1045	1050	1055
250	Val Leu Lys His Leu Thr Ala Leu Ile Lys Ser Gln Glu Lys Val Gly		
251	1060	1065	1070
252	Ile Val Gly Arg Thr Gly Ala Gly Lys Ser Ser Leu Ile Ser Ala Leu		
253	1075	1080	1085
254	Phe Arg Leu Ser Glu Pro Glu Gly Lys Ile Trp Ile Asp Lys Ile Leu		
255	1090	1095	1100
256	Thr Thr Glu Ile Gly Leu His Asp Leu Arg Lys Lys Met Ser Ile Ile		
257	1105	1110	1115
			1120

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 06/23/2003  
PATENT APPLICATION: US/09/647,140B TIME: 14:00:59

Input Set : A:\Kruh 140 SequenceListing v2.txt  
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**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; N Pos. 18  
Seq#:16; N Pos. 4,7,10,13,16,19  
Seq#:17; N Pos. 23,29  
Seq#:18; N Pos. 9,18